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T, 1920

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 Ser Pro Gly Asn Met Glu Arg Ile Val Ile Cys Leu Met Val Ile Phe
 5 10 15

ttg ggg aca ctg gtc cac aaa tca agc tcc caa ggt caa gat cgc cac 151
 Leu Gly Thr Leu Val His Lys Ser Ser Ser Gln Gly Gln Asp Arg His
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atg att aga atg cgt caa ctt ata gat att gtt gat cag ctg aaa aat 199
 Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp Gln Leu Lys Asn
 40 45 50

tat gtg aat gac ttg gtc cct gaa ttt ctg cca gct cca gaa gat gta 247
 Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro Glu Asp Val
 55 60 65

gag aca aac tgt gag tgg tca gct ttt tcc tgt ttt cag aag gcc caa 295
 Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln Lys Ala Gln
 70 75 80

cta aag tca gca aat aca gga aac aat gaa agg ata atc aat gta tca 343
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 85 90 95

att aaa aag ctg aag agg aaa cca cct tcc aca aat gca ggg aga aga 391
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 100 105 110 115

cag aaa cac aga cta aca tgc cct tca tgt gat tct tat gag aaa aaa 439
 Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr Glu Lys Lys
 120 125 130

cca ccc aaa gaa ttc cta gaa aga ttc aaa tca ctt ctc caa aag atg 487
 Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu Gln Lys Met
 135 140 145

att cat cag cat ctg tcc tct aga aca cac gga agt gaa gat tcc 532
 Ile His Gln His Leu Ser Ser Arg Thr His Gly Ser Glu Asp Ser
 150 155 160

tgaggatcta acttgcagtt ggacactatg ttacatactc taatatagta gtgaaagtca 592
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<213> Homo sapiens

[illegible]

<211> 486

<213> Artificial Sequence

<223> Degenerate polynucleotide sequence for human
zalpall ligand

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$\langle 223 \rangle$ n = A, T, C or G

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| atgmgwnsw | sncnggnaa | yatggarmgn | athgtnatht | gytntatggt | nathttyytn | 60 |
| ggnacnytn | tncaaarws | nwnwnsncar | ggncargaym | gncayatgat | hmgntatgmgn | 120 |
| carytnathg | ayathgtnga | ycarytnaar | aaytaygtna | aygayytngt | nccngartty | 180 |
| ytncngcnc | cngargaygt | ngaracnaay | tgygartggw | sngcnttyws | ntgyttycar | 240 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| aargncary | tnaarwsngc | naayacnggn | aayaaygarm | gnathathaa | ygtwnsnath | 300 |
| aaraarytna | armgnaarcc | nccnwsnacn | aaygcnggnm | gnmgncaraa | rcaymgnytn | 360 |
| acntgyccnw | sntgygayws | ntaygaraar | aarccnccna | argarttyyt | ngarmgntty | 420 |
| aarwsnytny | tncaraarat | gathcaycar | cayytnwsnw | snmgnacnca | yggwnsngar | 480 |
| gaywsn | | | | | | 486 |

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 <213> Mus musculus

<220>
 <221> source
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| atttataata | cttataatat | cattgttttg | ttcactaata | aatctatgga | tacatgggtca | 120 |
| aaatggaaat | gaatattttg | ccaattatta | atccccaag | tcattgaaaa | taagcataac | 180 |
| cattctactg | acttggttaga | ctctaaacta | acataaaaata | cattttcaga | aataaattca | 240 |
| accgatctta | cctttacatc | ttgtggagct | gatagaagtt | caggatccta | agaaaattaa | 300 |
| caaagagta | ttagttctga | gttggtgata | caagtcaaaa | ggctcctttt | gcattaatta | 360 |
| aaaaaatatt | atttaaattg | cattgtgaca | aacatggcct | taccaagtca | ttttcataga | 420 |
| ttttcagctg | ttcaacaatg | tcaataaggt | gacgaagtct | aatcaggagg | cgatctggcc | 480 |
| cttgggggct | tgatttatgg | gccactgtcc | ccaagaagat | gactaccaga | cagac | 535 |

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 <211> 33
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| <400> 5 | | | | | | |
| ggggaattcg | aagccatgcc | ctcttgggcc | ctc | | | 33 |

<210> 6
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC19914

30

 $\langle 400 \rangle$ 7

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| cccgaacctg | tctgtctacac | cgattacctc | cagacggtca | tctgcatcct | ggaaatgtgg | 120 |
| aacctccacc | ccagcacgct | cacccttacc | tggcaagacc | agtatgaaga | gctgaaggac | 180 |
| gaggccacct | cctgcagcct | ccacaggtcg | gccacaatg | ccacgcgatgc | cacctacacc | 240 |
| tgccacatgg | atgtattcca | cttcatggcc | gacgacattt | tcagtgtcaa | catcacagac | 300 |
| cagtctggca | actactcca | ggagtgtggc | agctttctcc | tggctgagag | catcaagccg | 360 |
| gctccccctt | tcaacgtgac | tgtgaccttc | tcaggacagt | ataatatctc | ctggcgctca | 420 |
| gattacgaag | accctgcctt | ctacatgctg | aagggaagc | ttcagtatga | gctgcagtac | 480 |
| aggaaccggg | gagacccctg | ggctgtgagt | ccgaggagaa | agctgatctc | agtggactca | 540 |
| agaagtgtct | ccctcctccc | cctggagttc | cgcaaagact | cgagctatga | gctgcagggtg | 600 |
| cgggcagggc | ccatgcctgg | ctcctcttac | caggggacct | ggagtgaatg | gagtgacccg | 660 |
| gtcatctttc | agaccagtc | agaggagtta | aaggaaggct | ggaaccctca | cctgctgctt | 720 |
| ctcctcctgc | ttgtcatagt | cttcattcct | gccttctgga | gcctgaagac | ccatccattg | 780 |
| tggaggctat | ggaagaagat | atgggccgtc | cccagccctg | agcggttctt | catgcccctg | 840 |
| tacaagggtc | gcagcggaga | cttcaagaaa | tgggtgggtg | cacccttcac | tggctccagc | 900 |
| ctggagctgg | gaccctggag | cccagaggtg | ccctccacc | tggaggtgta | cagctgccac | 960 |
| ccaccacgga | gcccggccaa | gaggctgcag | ctcacggagc | tacaagaacc | agcagagctg | 1020 |
| gtggagtctg | acggtgtgcc | caagcccagc | ttctggccga | cagcccagaa | ctcggggggc | 1080 |
| tcagcttaca | gtgaggagag | ggatcggcc | tacggcctgg | tgtccattga | cacagtgact | 1140 |
| gtgctagatg | agagggggcc | atgcacctgg | ccctgcagct | gtgaggatga | cggctaccca | 1200 |
| gccctggacc | tggatgctgg | cctggagccc | agcccaggcc | tagaggaccc | actcttggat | 1260 |
| gcagggacca | cagtctgtc | ctgtggctgt | gtctcagctg | gcagccctgg | gctaggaggg | 1320 |
| cccctgggaa | gcctcctgga | cagactaaa | ccacccttg | cagatgggga | ggactgggct | 1380 |
| gggggactgc | cctgggggtg | ccggtcacct | ggaggggtct | cagagagtga | ggcgggctca | 1440 |
| cccctggccg | gcctggatat | ggacacgttt | gacagtggct | ttgtgggctc | tgactgcagc | 1500 |
| agccctgtgg | agtgtgactt | caccagcccc | ggggacgaag | gacccccccg | gagctacctc | 1560 |
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<223> Oligonucleotide primer ZC6675

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<400> 13
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<210> 14
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<400> 14
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21

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18

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<211> 24

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<220>
 <223> Glu-Glu (CEE) Tag amino acid sequence

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 1 5

<210> 30
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<210> 32
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 region and the 5' end of the zalphal1
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ggccgc

66

<210> 33
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| ggggcaccgt | cagtcttct | cttcccccca | aaaccaagg | acaccctcat | gatctcccgg | 120 |
| acccttgagg | tcacatgct | ggtggtggac | gtgagccacg | aagaccctga | ggtcaagttc | 180 |
| aactggtacg | tggacggcgt | ggaggtgcat | aatgccaaga | caaagccgcg | ggaggagcag | 240 |
| tacaacagca | cgtaccgtgt | ggtcagcgtc | ctcaccgtcc | tgcaccagga | ctggctgaat | 300 |
| ggcaaggagt | acaagtgcaa | ggtctccaac | aaagccctcc | catcctccat | cgagaaaacc | 360 |
| atctccaaag | ccaaagggca | gccccgagaa | ccacaggtgt | acaccctgcc | cccatcccgg | 420 |
| gatgagctga | ccaagaacca | ggtcagcctg | acctgcctgg | tcaaaggctt | ctatcccagc | 480 |
| gacatcgccg | tggagtggga | gagcaatggg | cagccggaga | acaactacaa | gaccacgcct | 540 |
| cccgtgctgg | actccgacgg | ctccttcttc | ctctacagca | agctcaccgt | ggacaagagc | 600 |
| aggtggcagc | aggggaacgt | cttctcatgc | tccgtgatgc | atgaggctct | gcacaaccac | 660 |
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<223> First Oligonucleotide primer spanning 3' end of
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 of Fc4

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| gcacggtggg | catgtgtgag | ttttgtctga | agatctgggc | tcgtgagggt | tccagccttc | 60 |
| ct | | | | | | 62 |

<210> 35
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<220>

<223> Second Oligonucleotide primer spanning 3' end of
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 of Fc4

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<210> 37
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<220>
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26

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<211> 16

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Glu Arg Thr Leu Val Cys Leu Val Val Ile Phe Leu Gly Thr Val Ala
5 10 15

cat aaa tca agc ccc caa ggg cca gat cgc ctc ctg att aga ctt cgt 152
His Lys Ser Ser Pro Gln Gly Pro Asp Arg Leu Leu Ile Arg Leu Arg
20 25 30

cac ctt att gac att gtt gaa cag ctg aaa atc tat gaa aat gac ttg 200
His Leu Ile Asp Ile Val Glu Gln Leu Lys Ile Tyr Glu Asn Asp Leu
35 40 45

gat cct gaa ctt cta tca gct cca caa gat gta aag ggg cac tgt gag 248
Asp Pro Glu Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys Glu
50 55 60 65

cat gca gct ttt gcc tgt ttt cag aag gcc aaa ctc aag cca tca aac 296
His Ala Ala Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser Asn
70 75 80

cct gga aac aat aag aca ttc atc att gac ctc gtg gcc cag ctc agg 344
Pro Gly Asn Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu Arg
85 90 95

agg agg ctg cct gcc agg agg gga gga aag aaa cag aag cac ata gct 392
Arg Arg Leu Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile Ala
100 105 110

aaa tgc cct tcc tgt gat tcg tat gag aaa agg aca ccc aaa gaa ttc 440
Lys Cys Pro Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu Phe
115 120 125

cta gaa aga cta aaa tgg ctc ctt caa aag atg att cat cag cat ctc 488
Leu Glu Arg Leu Lys Trp Leu Leu Gln Lys Met Ile His Gln His Leu
130 135 140 145

tcc tagaacacat aggacccgaa gattcctgag gatccgagaa gattcccagag 541
Ser

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<213> mus musculus

<400> 56

[illegible]

<211> 34

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34

<211> 31

<213> Artificial Sequence

<223> Oligonucleotide primer ZC22284

<400> 58

gctctagaat cttctcggat cctcaggaat c

31

<210> 59

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<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC12749

<400> 59

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aactgtagat ttctaggaat tcaatccttg gccacgcgtc 100

<210> 60

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC12748

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cgcgtgtgta attccgggaa ggggagggat ttacgggaag 100

<210> 61

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC22143

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cgtatcggcc ggccaccatg agatccagtc ct 32

<210> 62

<211> 32

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC22144

<400> 62
cgctacgggcg cgcctcagga atcttcactt cc 32

<210> 63
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atagatatggt ttgatcagct gaaaaattat gtgaatgact tggccctga atttctgcca 180
gctccagaag atgtagagac aaactgtgag tggtcagctt tttcctgttt tcagaaggcc 240
caactaaagt cagcaaatac aggaacaat gaaaggataa tcaatgtatc aattaaaaag 300
ctgaagagga aaccaccttc cacaaatgca gggagaagac agaaacacag actaacatgc 360
ccttcattgtg attcttatga gaaaaaacca cccaaagaat tcctagaaag attcaaatca 420
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tga 483

<210> 64
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC22052

<400> 64
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<210> 65
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<212> DNA
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<400> 65
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<210> 66
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<223> Oligonucleotide primer ZC23115

<400> 66

gtatacggcc ggccaccatg gagaggaccc tt

32

<210> 67

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC23116

<400> 67

cgtatcggcg cgccctagga gagatgctga tg

32

<210> 68

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC20892

<400> 68

gtatacggtt aaacgccacc atgccgcgtg gctgg

35

<210> 69

<211> 32

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC20893

<400> 69

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32

<210> 70

<211> 39

<212> DNA

<213> Artificial Sequence

214

006030-2722560

<223> Oligonucleotide primer ZC22054

cccgggggtcg acaccatgga ttccagtcct ggcaacatg

39

<211> 32

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<223> Oligonucleotide primer ZC22055

tgcagtttaa actcaggaat cttcacttcc gt

32

<211> 40

<213> Artificial Sequence

<223> Huza1pha11L-1 peptide

Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp
1 5 10 15
Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala
20 25 30
Pro Glu Asp Val Glu Thr Asn Cys
35 40

<211> 32

<213> Artificial Sequence

<223> Huza1pha11L-3 peptide

Cys Pro Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu
1 5 10 15

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| <210> 74 | |
| <211> 29 | |
| <212> DNA | |
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| <220> | |
| <223> Oligonucleotide primer ZC23444 | |
| <400> 74 | |
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| <210> 75 | |
| <211> 32 | |
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| <223> Oligonucleotide primer ZC23445 | |
| <400> 75 | |
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| <223> Oligonucleotide primer ZC447 | |
| <400> 76 | |
| taacaatttc acacagg | 17 |
| <210> 77 | |
| <211> 18 | |
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| <223> Oligonucleotide primer ZC976 | |
| <400> 77 | |

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<210> 82
<211> 60
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<220>
<223> Oligonucleotide primer ZC19352

<400> 82
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<210> 83
<211> 42
<212> DNA
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<223> Oligonucleotide primer ZC19371

<400> 83
acggccagtg aattgtaata cgactcacta tagggcgaat tg 42

<210> 84
<211> 1560
<212> DNA
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<220>
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<222> (1)...(1560)

<223> MBP-human zalpha11 Ligand fusion polynucleotide

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Met Lys Thr Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
1 5 10 15

ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat acc 96
Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
20 25 30

219

| | |
|---|------|
| acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca gcg | 672 |
| Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala | |
| 210 215 220 | |
| atg acc atc aac ggc ccg tgg gca tgg tcc aac atc gac acc agc aaa | 720 |
| Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys | |
| 225 230 235 240 | |
| gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca tcc | 768 |
| Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser | |
| 245 250 255 | |
| aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt ccg | 816 |
| Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro | |
| 260 265 270 | |
| aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act gat | 864 |
| Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp | |
| 275 280 285 | |
| gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta gcg | 912 |
| Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala | |
| 290 295 300 | |
| ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc gcc | 960 |
| Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala | |
| 305 310 315 320 | |
| acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg cag | 1008 |
| Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln | |
| 325 330 335 | |
| atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc gcc | 1056 |
| Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala | |
| 340 345 350 | |
| agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act aat | 1104 |
| Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn | |
| 355 360 365 | |
| tcg agc tcc cac cat cac cat cac cac gcg aat tcg gta ccg ctg gtt | 1152 |
| Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val | |
| 370 375 380 | |

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<210> 85
<211> 519
<212> PRT
<213> Artificial Sequence

<220>
<223> MBP-human zalpha11 Ligand fusion polypeptide
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| Met
1 | Lys | Thr | Glu | Glu | Gly | Lys | Leu | Val | Ile | Trp | Ile | Asn | Gly | Asp | Lys |
| Gly | Tyr | Asn | Gly | Leu | Ala | Glu | Val | Gly | Lys | Lys | Phe | Glu | Lys | Asp | Thr |
| Gly | Ile | Lys | Val | Thr | Val | Glu | His | Pro | Asp | Lys | Leu | Glu | Glu | Lys | Phe |
| Pro | Gln | Val | Ala | Ala | Thr | Gly | Asp | Gly | Pro | Asp | Ile | Ile | Phe | Trp | Ala |
| His | Asp | Arg | Phe | Gly | Gly | Tyr | Ala | Gln | Ser | Gly | Leu | Leu | Ala | Glu | Ile |
| Thr | Pro | Asp | Lys | Ala | Phe | Gln | Asp | Lys | Leu | Tyr | Pro | Phe | Thr | Trp | Asp |
| Ala | Val | Arg | Tyr | Asn | Gly | Lys | Leu | Ile | Ala | Tyr | Pro | Ile | Ala | Val | Glu |
| Ala | Leu | Ser | Leu | Ile | Tyr | Asn | Lys | Asp | Leu | Leu | Pro | Asn | Pro | Pro | Lys |
| Thr | Trp | Glu | Glu | Ile | Pro | Ala | Leu | Asp | Lys | Glu | Leu | Lys | Ala | Lys | Gly |
| Lys | Ser | Ala | Leu | Met | Phe | Asn | Leu | Gln | Glu | Pro | Tyr | Phe | Thr | Trp | Pro |
| Leu | Ile | Ala | Ala | Asp | Gly | Gly | Tyr | Ala | Phe | Lys | Tyr | Glu | Asn | Gly | Lys |
| Tyr | Asp | Ile | Lys | Asp | Val | Gly | Val | Asp | Asn | Ala | Gly | Ala | Lys | Ala | Gly |
| Leu | Thr | Phe | Leu | Val | Asp | Leu | Ile | Lys | Asn | Lys | His | Met | Asn | Ala | Asp |
| Thr | Asp | Tyr | Ser | Ile | Ala | Glu | Ala | Ala | Phe | Asn | Lys | Gly | Glu | Thr | Ala |
| Met | Thr | Ile | Asn | Gly | Pro | Trp | Ala | Trp | Ser | Asn | Ile | Asp | Thr | Ser | Lys |
| Val | Asn | Tyr | Gly | Val | Thr | Val | Leu | Pro | Thr | Phe | Lys | Gly | Gln | Pro | Ser |
| Lys | Pro | Phe | Val | Gly | Val | Leu | Ser | Ala | Gly | Ile | Asn | Ala | Ala | Ser | Pro |
| Asn | Lys | Glu | Leu | Ala | Lys | Glu | Phe | Leu | Glu | Asn | Tyr | Leu | Leu | Thr | Asp |
| Glu | Gly | Leu | Glu | Ala | Val | Asn | Lys | Asp | Lys | Pro | Leu | Gly | Ala | Val | Ala |
| Leu | Lys | Ser | Tyr | Glu | Glu | Glu | Leu | Ala | Lys | Asp | Pro | Arg | Ile | Ala | Ala |
| Thr | Met | Glu | Asn | Ala | Gln | Lys | Gly | Glu | Ile | Met | Pro | Asn | Ile | Pro | Gln |
| Met | Ser | Ala | Phe | Trp | Tyr | Ala | Val | Arg | Thr | Ala | Val | Ile | Asn | Ala | Ala |

Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365
 Ser Ser Ser His His His His His Ala Asn Ser Val Pro Leu Val
 370 375 380
 Pro Arg Gly Ser Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile
 385 390 395 400
 Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu
 405 410 415
 Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala
 420 425 430
 Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn
 435 440 445
 Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro
 450 455 460
 Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro
 465 470 475 480
 Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg
 485 490 495
 Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg
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 Thr His Gly Ser Glu Asp Ser
 515

<210> 86

<211> 64

<212> DNA

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<223> Oligonucleotide primer ZC22849

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actt

60

64

<210> 87

<211> 64

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<223> Oligonucleotide primer ZC22850

<400> 87

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64

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<221> CDS
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1 5 10 15

ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat acc 96
Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
20 25 30

gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa ttc 144
Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
35 40 45

cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg gca 192
Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
50 55 60

cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa atc 240
His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
65 70 75 80

acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg gat 288
Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
85 90 95

gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt gaa 336
Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
100 105 110

gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca aaa 384
Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
115 120 125

२२५

226

tcc tgt gat tcg tat gag aaa agg aca ccc aaa gaa ttc cta gaa aga 1488
 Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu Phe Leu Glu Arg
 485 490 495

cta aaa tgg ctc ctt caa aag atg att cat cag cat ctc tcc tga 1533
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<210> 89

<211> 510

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP-mouse zalphal1 Ligand fusion polypeptide

<400> 89

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Thr | Glu | Gly | Lys | Leu | Val | Ile | Trp | Ile | Asn | Gly | Asp | Lys | 1 | 5 | 10 | 15 |
| Gly | Tyr | Asn | Gly | Leu | Ala | Glu | Val | Gly | Lys | Lys | Phe | Glu | Lys | Asp | Thr | 20 | 25 | 30 |
| Gly | Ile | Lys | Val | Thr | Val | Glu | His | Pro | Asp | Lys | Leu | Glu | Glu | Lys | Phe | 35 | 40 | 45 |
| Pro | Gln | Val | Ala | Ala | Thr | Gly | Asp | Gly | Pro | Asp | Ile | Ile | Phe | Trp | Ala | 50 | 55 | 60 |
| His | Asp | Arg | Phe | Gly | Gly | Tyr | Ala | Gln | Ser | Gly | Leu | Leu | Ala | Glu | Ile | 65 | 70 | 75 |
| Thr | Pro | Asp | Lys | Ala | Phe | Gln | Asp | Lys | Leu | Tyr | Pro | Phe | Thr | Trp | Asp | 85 | 90 | 95 |
| Ala | Val | Arg | Tyr | Asn | Gly | Lys | Leu | Ile | Ala | Tyr | Pro | Ile | Ala | Val | Glu | 100 | 105 | 110 |
| Ala | Leu | Ser | Leu | Ile | Tyr | Asn | Lys | Asp | Leu | Leu | Pro | Asn | Pro | Pro | Lys | 115 | 120 | 125 |
| Thr | Trp | Glu | Glu | Ile | Pro | Ala | Leu | Asp | Lys | Glu | Leu | Lys | Ala | Lys | Gly | 130 | 135 | 140 |
| Lys | Ser | Ala | Leu | Met | Phe | Asn | Leu | Gln | Glu | Pro | Tyr | Phe | Thr | Trp | Pro | 145 | 150 | 155 |
| Leu | Ile | Ala | Ala | Asp | Gly | Gly | Tyr | Ala | Phe | Lys | Tyr | Glu | Asn | Gly | Lys | 165 | 170 | 175 |
| Tyr | Asp | Ile | Lys | Asp | Val | Gly | Val | Asp | Asn | Ala | Gly | Ala | Lys | Ala | Gly | 180 | 185 | 190 |
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228

<400> 90

22

<211> 23

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<223> Oligonucleotide primer ZC22279

<400> 91

23

<210> 92

<211> 31

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Human zalpha11 Ligand TaqMan probe, ZG32

<400> 92

31

<210> 93

<211> 20

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Oligonucleotide primer ZC22277

<400> 93

20

<210> 94

$\langle 211 \rangle$ 21

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Oligonucleotide primer ZC22276

<400> 94

<211> 23

<213> Artificial Sequence

<223> Human za1pha11 TaqMan probe, ZG31

<400> 95

<211> 1821

<213> Artificial Sequence

<221> CDS

<222> (1)...(1821)

<223> MBP-zalpha11 soluble receptor polynucleotide
sequence

<400> 96

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Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
20 25 30

gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa ttc
Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
35 40 45

cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg gca
Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
50 55 60

| | |
|---|-----|
| cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa atc | 240 |
| His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile | |
| 65 70 75 80 | |
| acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg gat | 288 |
| Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp | |
| 85 90 95 | |
| gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt gaa | 336 |
| Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu | |
| 100 105 110 | |
| gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca aaa | 384 |
| Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys | |
| 115 120 125 | |
| acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa ggt | 432 |
| Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly | |
| 130 135 140 | |
| aag agc gcg ctg atg ttc aac ctg caa gaa ccg tac ttc acc tgg ccg | 480 |
| Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro | |
| 145 150 155 160 | |
| ctg att gct gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc aag | 528 |
| Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys | |
| 165 170 175 | |
| tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg ggt | 576 |
| Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly | |
| 180 185 190 | |
| ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca gac | 624 |
| Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp | |
| 195 200 205 | |
| acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca gcg | 672 |
| Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala | |
| 210 215 220 | |
| atg acc atc aac ggc ccg tgg gca tgg tcc aac atc gac acc agc aaa | 720 |
| Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys | |
| 225 230 235 240 | |

| | |
|---|------|
| gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca tcc | 768 |
| Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser | |
| 245 250 255 | |
| aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt ccg | 816 |
| Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro | |
| 260 265 270 | |
| aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act gat | 864 |
| Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp | |
| 275 280 285 | |
| gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta gcg | 912 |
| Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala | |
| 290 295 300 | |
| ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc gcc | 960 |
| Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala | |
| 305 310 315 320 | |
| acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg cag | 1008 |
| Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln | |
| 325 330 335 | |
| atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc gcc | 1056 |
| Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala | |
| 340 345 350 | |
| agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act aat | 1104 |
| Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn | |
| 355 360 365 | |
| tcg agc tcc cac cat cac cat cac cac gcg aat tcg gta ccg ctg gtt | 1152 |
| Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val | |
| 370 375 380 | |
| ccg cgt gga tcc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag | 1200 |
| Pro Arg Gly Ser Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln | |
| 385 390 395 400 | |
| acg gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc | 1248 |
| Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu | |
| 405 410 415 | |

| | |
|---|------|
| acc ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc | 1296 |
| Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr | |
| 420 425 430 | |
| tcc tgc agc ctc cac agg tcg gcc cac aat gcc acg cat gcc acc tac | 1344 |
| Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr | |
| 435 440 445 | |
| acc tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt | 1392 |
| Thr Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser | |
| 450 455 460 | |
| gtc aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc | 1440 |
| Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser | |
| 465 470 475 480 | |
| ttt ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act | 1488 |
| Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr | |
| 485 490 495 | |
| gtg acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa | 1536 |
| Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu | |
| 500 505 510 | |
| gac cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag | 1584 |
| Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln | |
| 515 520 525 | |
| tac agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg | 1632 |
| Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu | |
| 530 535 540 | |
| atc tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc | 1680 |
| Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg | |
| 545 550 555 560 | |
| aaa gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc | 1728 |
| Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly | |
| 565 570 575 | |
| tcc tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt | 1776 |
| Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe | |
| 580 585 590 | |

1821

<210> 97
<211> 606
<212> PRT
<213> Artificial Sequence

<220>
<223> MBP-zalpha11 soluble receptor polypeptide sequence

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| | <400> | | | | | | | | | | | | | | 97 |
| Met
1 | Lys | Ile | Glu | Glu
5 | Gly | Lys | Leu | Val | Ile
10 | Trp | Ile | Asn | Gly | Asp
15 | Lys |
| Gly | Tyr | Asn | Gly
20 | Leu | Ala | Glu | Val | Gly
25 | Lys | Lys | Phe | Glu | Lys
30 | Asp | Thr |
| Gly | Ile | Lys
35 | Val | Thr | Val | Glu | His
40 | Pro | Asp | Lys | Leu | Glu | Glu
45 | Lys | Phe |
| Pro | Gln | Val | Ala | Ala | Thr | Gly
55 | Asp | Gly | Pro | Asp | Ile
60 | Ile | Phe | Trp | Ala |
| His
65 | Asp | Arg | Phe | Gly
70 | Gly | Tyr | Ala | Gln | Ser | Gly
75 | Leu | Leu | Ala | Glu
80 | Ile |
| Thr | Pro | Asp | Lys
85 | Ala | Phe | Gln | Asp | Lys
90 | Leu | Tyr | Pro | Phe | Thr
95 | Trp | Asp |
| Ala | Val | Arg | Tyr
100 | Asn | Gly | Lys | Leu | Ile
105 | Ala | Tyr | Pro | Ile | Ala
110 | Val | Glu |
| Ala | Leu | Ser
115 | Leu | Ile | Tyr | Asn
120 | Lys | Asp | Leu | Leu | Pro | Asn
125 | Pro | Pro | Lys |
| Thr | Trp
130 | Glu | Glu | Ile | Pro | Ala
135 | Leu | Asp | Lys | Glu | Leu
140 | Lys | Ala | Lys | Gly |
| Lys
145 | Ser | Ala | Leu | Met
150 | Phe | Asn | Leu | Gln | Glu | Pro | Tyr
155 | Phe | Thr | Trp | Pro |
| Leu | Ile | Ala | Ala | Asp
165 | Gly | Gly | Tyr | Ala | Phe
170 | Lys | Tyr | Glu | Asn
175 | Gly | Lys |
| Tyr | Asp | Ile
180 | Lys | Asp | Val | Gly | Val | Asp
185 | Asn | Ala | Gly | Ala
190 | Lys | Ala | Gly |
| Leu | Thr | Phe
195 | Leu | Val | Asp | Leu | Ile
200 | Lys | Asn | Lys | His
205 | Met | Asn | Ala | Asp |
| Thr | Asp
210 | Tyr | Ser | Ile | Ala | Glu
215 | Ala | Ala | Phe | Asn | Lys
220 | Gly | Glu | Thr | Ala |
| Met
225 | Thr | Ile | Asn | Gly
230 | Pro | Trp | Ala | Trp | Ser | Asn
235 | Ile | Asp | Thr | Ser | Lys |

234

235

Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His
 595 600 605

<210> 98
 <211> 65
 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC20187

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 caccg 65

<210> 99
 <211> 68
 <212> DNA
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<220>
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 cctttaac 68

<210> 100
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<220>
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<400> 100
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<210> 101
 <211> 21
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<220>
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<400> 101

<211> 21

<213> Art

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<400> 102

<211> 23

<213> Art:

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<211> 18

<213> Art-

<223> Oligonucleotide primer ZC23771

$\langle 400 \rangle$ 104

<211> 1347

<213> Homo sapiens

<400> 105

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ccatcaatcc  ctgccccac  acattagcac  atgcacacgt  atacctagcc  agtggaaaag     120
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<210> 106
<211> 1656
<212> DNA
<213> Homo sapiens
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238

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<211> 644
<212> DNA
<213> Homo sapiens
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<212> DNA
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239

<210> 109
<211> 36
<212> DNA
<213> Artificial Sequence

<400> 109
tcta gactaggaga gatgctgatg aatcat 36

<220>
<223> Oligonucleotide primer ZC25969

<400> 110
atgcattccg gacataaatc aagcccccaa gggcca 36

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<210> 111
<211> 153
<212> PRT
<213> Homo sapiens
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| <400> 111 | | | | | | | | | | | | | | | |
| Met | Tyr | Arg | Met | Gln | Leu | Leu | Ser | Cys | Ile | Ala | Leu | Ser | Leu | Ala | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Thr | Asn | Ser | Ala | Pro | Thr | Ser | Ser | Ser | Thr | Lys | Lys | Thr | Gln | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gln | Leu | Glu | His | Leu | Leu | Leu | Asp | Leu | Gln | Met | Ile | Leu | Asn | Gly | Ile |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Asn | Asn | Tyr | Lys | Asn | Pro | Lys | Leu | Thr | Arg | Met | Leu | Thr | Phe | Lys | Phe |
| | 50 | | | | | 55 | | | | | 60 | | | | |

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<210> 112
<211> 153
<212> PRT
<213> Homo sapiens
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[illegible]

<211> 144

<213> Home

<213> Homo sapiens

| | | | | | | | | | | | | | | | |
|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----|
| Met
1 | Trp | Leu | Gln | Ser
5 | Leu | Leu | Leu | Leu | Gly
10 | Thr | Val | Ala | Cys | Ser
15 | Ile |
| Ser | Ala | Pro | Ala
20 | Arg | Ser | Pro | Ser | Pro
25 | Ser | Thr | Gln | Pro | Trp
30 | Glu | His |
| Val | Asn | Ala
35 | Ile | Gln | Glu | Ala | Arg
40 | Arg | Leu | Leu | Asn | Leu
45 | Ser | Arg | Asp |
| Thr | Ala
50 | Ala | Glu | Met | Asn | Glu
55 | Thr | Val | Glu | Val | Ile
60 | Ser | Glu | Met | Phe |
| Asp
65 | Leu | Gln | Glu | Pro | Thr
70 | Cys | Leu | Gln | Thr | Arg
75 | Leu | Glu | Leu | Tyr
80 | Lys |
| Gln | Gly | Leu | Arg | Gly
85 | Ser | Leu | Thr | Lys
90 | Leu | Lys | Gly | Pro | Leu
95 | Thr | Met |
| Met | Ala | Ser | His
100 | Tyr | Lys | Gln | His | Cys
105 | Pro | Pro | Thr | Pro | Glu
110 | Thr | Ser |

Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
 115 120 125
 Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
 130 135 140

<210> 115
 <211> 538
 <212> PRT
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<400> 115

Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Leu Gln Gly
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 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
 20 25 30
 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
 35 40 45
 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
 50 55 60
 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
 65 70 75 80
 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
 85 90 95
 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
 100 105 110
 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
 115 120 125
 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
 130 135 140
 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
 145 150 155 160
 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
 165 170 175
 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
 180 185 190
 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
 195 200 205
 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 210 215 220
 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu
 225 230 235 240
 Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys
 245 250 255
 Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser
 260 265 270

Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe
 275 280 285
 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly
 290 295 300
 Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His
 305 310 315 320
 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu
 325 330 335
 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp
 340 345 350
 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp
 355 360 365
 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala
 370 375 380
 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
 385 390 395 400
 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
 405 410 415
 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser
 420 425 430
 Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg
 435 440 445
 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro
 450 455 460
 Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser
 465 470 475 480
 Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly
 485 490 495
 Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp
 500 505 510
 Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro
 515 520 525
 Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
 530 535